

SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> A NOVEL HUMAN LEUCINE-RICH REPEAT CONTAINING PROTEIN EXPRESSED PREDOMINATELY IN BONE MARROW, HLRRBM1

<130> D0067NP

<150> US 60/257,773

<151> 2000-12-22

<160> 22

<170> PatentIn version 3.0

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Pro Gly Ala Pro Arg Leu Gln Pro Pro Pro Asn Gln Arg Gly Leu Cys	195	200	205
Ser Leu Ala Ala Asp Gly Leu Trp Asn Gln Lys Ile Leu Phe Glu Glu	210	215	220
Gln Asp Leu Arg Lys His Gly Leu Asp Gly Glu Asp Val Ser Ala Phe	225	230	235
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Arg Ser His Leu Glu Lys Ser Leu Cys Trp Lys Val Ser Pro His Ile	275	280	285
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Ile Val Val Ser Asn Ile Ala Ser Lys Met Glu His Met Val Ser Ser	340	345	350
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Ala Tyr Ser Glu His Leu Ala Ala Ala Leu Cys Thr Asn Pro Asn Leu
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Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
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Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
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Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
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Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys
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Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser
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Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser His Leu Tyr Gln Ala Leu
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Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala
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 Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
 225 230 235 240
 Pro Pro Gln Ala His Ser Ser Leu Gln Pro His His His Pro Trp Glu
 245 250 255
 Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu
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 Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val
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 Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser
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 Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser
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 Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly
 405 410 415
 Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln
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515

520

525

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Lys Thr Thr Thr Thr Leu Cys Leu His Tyr Leu Ala Gln Ala Leu Gln
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565 570 575

Glu Gly Ile Trp Gln Lys Lys Thr Leu Phe Ser Pro Asp Asp Leu Arg
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Lys His Gly Leu Asp Gly Ala Ile Ile Ser Thr Phe Leu Lys Met Gly
595 600 605

Ile Leu Gln Glu His Pro Ile Pro Leu Ser Tyr Ser Phe Ile His Leu
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Cys Phe Gln Glu Phe Phe Ala Ala Met Ser Tyr Val Leu Glu Asp Glu
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Ile Phe His Cys Arg Leu Ser Gln Gly Arg Asn Leu Met Gln Trp Val
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725 730 735

His Phe Glu Glu Met Gly Met Cys Val Glu Thr Asp Met Glu Leu Leu
740 745 750

Val Cys Thr Phe Cys Ile Lys Phe Ser Arg His Val Lys Lys Leu Gln
755 760 765

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850 855 860

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Ser

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Tyr Phe Ser Ala Glu Asp Ala Glu Ile Val Cys Ala Cys Pro Thr Gln
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Tyr Val Asp Leu Arg Pro Trp Leu Leu Glu Ile Gly Phe Ser Pro Ser
100 105 110

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Asp Ala Gly Val Lys Phe Phe Phe His Phe Arg Cys Arg Met Phe Ser
225 230 235 240

Cys Phe Lys Glu Ser Asp Arg Leu Cys Leu Gln Asp Leu Leu Phe Lys
245 250 255

His Tyr Cys Tyr Pro Glu Arg Asp Pro Glu Glu Val Phe Ala Phe Leu
260 265 270

Leu Arg Phe Pro His Val Ala Leu Phe Thr Phe Asp Gly Leu Asp Glu
275 280 285

Leu His Ser Asp Leu Asp Leu Ser Arg Val Pro Asp Ser Ser Cys Pro
290 295 300

Trp Glu Pro Ala His Pro Leu Val Leu Leu Ala Asn Leu Leu Ser Gly

305		310		315		320
Lys Leu Leu Lys	Gly Ala Ser Lys Leu Leu Thr Ala Arg Thr Gly Ile					
	325			330		335
Glu Val Pro Arg	Gln Phe Leu Arg Lys Lys Val Leu Leu Arg Gly Phe					
	340		345		350	
Ser Pro Ser His	Leu Arg Ala Tyr Ala Arg Arg Met Phe Pro Glu Arg					
	355		360		365	
Ala Leu Gln Asp	Arg Leu Leu Ser Gln Leu Glu Ala Asn Pro Asn Leu					
	370		375		380	
Cys Ser Leu Cys	Ser Val Pro Leu Phe Cys Trp Ile Ile Phe Arg Cys					
	385		390		395	400
Phe Gln His Phe	Arg Ala Ala Phe Glu Gly Ser Pro Gln Leu Pro Asp					
	405		410		415	
Cys Thr Met Thr	Leu Thr Asp Val Phe Leu Leu Val Thr Glu Val His					
	420		425		430	
Leu Asn Arg Met	Gln Pro Ser Ser Leu Val Gln Arg Asn Thr Arg Ser					
	435		440		445	
Pro Val Glu Thr	Leu His Ala Gly Arg Asp Thr Leu Cys Ser Leu Gly					
	450		455		460	
Gln Val Ala His	Arg Gly Met Glu Lys Ser Leu Phe Val Phe Thr Gln					
	465		470		475	480
Glu Glu Val Gln	Ala Ser Gly Leu Gln Glu Arg Asp Met Gln Leu Gly					
	485		490		495	
Phe Leu Arg Ala	Leu Pro Glu Leu Gly Pro Gly Gly Asp Gln Gln Ser					
	500		505		510	
Tyr Glu Phe Phe	His Leu Thr Leu Gln Ala Phe Phe Thr Ala Phe Phe					
	515		520		525	
Leu Val Leu Asp	Asp Arg Val Gly Thr Gln Glu Leu Leu Arg Phe Phe					
	530		535		540	
Gln Glu Trp Met	Pro Pro Ala Gly Ala Ala Thr Thr Ser Cys Tyr Pro					
	545		550		555	560
Pro Phe Leu Pro	Phe Gln Cys Leu Gln Gly Ser Gly Pro Ala Arg Glu					
	565		570		575	
Asp Leu Phe Lys	Asn Lys Asp His Phe Gln Phe Thr Asn Leu Phe Leu					
	580		585		590	
Cys Gly Leu Leu	Ser Lys Ala Lys Gln Lys Leu Leu Arg His Leu Val					
	595		600		605	
Pro Ala Ala Ala	Leu Arg Arg Lys Arg Lys Ala Leu Trp Ala His Leu					
	610		615		620	
Phe Ser Ser Leu	Arg Gly Tyr Leu Lys Ser Leu Pro Arg Val Gln Val					
	625		630		635	640

Glu Ser Phe Asn Gln Val Gln Ala Met Pro Thr Phe Ile Trp Met Leu
 645 650 655
 Arg Cys Ile Tyr Glu Thr Gln Ser Gln Lys Val Gly Gln Leu Ala Ala
 660 665 670
 Arg Gly Ile Cys Ala Asn Tyr Leu Lys Leu Thr Tyr Cys Asn Ala Cys
 675 680 685
 Ser Ala Asp Cys Ser Ala Leu Ser Phe Val Leu His His Phe Pro Lys
 690 695 700
 Arg Leu Ala Leu Asp Leu Asp Asn Asn Asn Leu Asn Asp Tyr Gly Val
 705 710 715 720
 Arg Glu Leu Gln Pro Cys Phe Ser Arg Leu Thr Val Leu Arg Leu Ser
 725 730 735
 Val Asn Gln Ile Thr Asp Gly Gly Val Lys Val Leu Ser Glu Glu Leu
 740 745 750
 Thr Lys Tyr Lys Ile Val Thr Tyr Leu Gly Leu Tyr Asn Asn Gln Ile
 755 760 765
 Thr Asp Val Gly Ala Arg Tyr Val Thr Lys Ile Leu Asp Glu Cys Lys
 770 775 780
 Gly Leu Thr His Leu Lys Leu Gly Lys Asn Lys Ile Thr Ser Glu Gly
 785 790 795 800
 Gly Lys Tyr Leu Ala Leu Ala Val Lys Asn Ser Lys Ser Ile Ser Glu
 805 810 815
 Val Gly Met Trp Gly Asn Gln Val Gly Asp Glu Gly Ala Lys Ala Phe
 820 825 830
 Ala Glu Ala Leu Arg Asn His Pro Ser Leu Thr Thr Leu Ser Leu Ala
 835 840 845
 Ser Asn Gly Ile Ser Thr Glu Gly Gly Lys Ser Leu Ala Arg Ala Leu
 850 855 860
 Gln Gln Asn Thr Ser Leu Glu Ile Leu Trp Leu Thr Gln Asn Glu Leu
 865 870 875 880
 Asn Asp Glu Val Ala Glu Ser Leu Ala Glu Met Leu Lys Val Asn Gln
 885 890 895
 Thr Leu Lys His Leu Trp Leu Ile Gln Asn Gln Ile Thr Ala Lys Gly
 900 905 910
 Thr Ala Gln Leu Ala Asp Ala Leu Gln Ser Asn Thr Gly Ile Thr Glu
 915 920 925
 Ile Cys Leu Asn Gly Asn Leu Ile Lys Pro Glu Glu Ala Lys Val Tyr
 930 935 940
 Glu Asp Glu Lys Arg Ile Ile Cys Phe
 945 950

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<210> 5
<211> 308
<212> DNA
<213> homo sapiens

<400> 5
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gtggatccaa agcaaagctc agagcgacgg ctccacctg cagcagggct cctttgagtt      120
cttcagttagc ttgtacgaga tccaggagga ggagtttacc cagcaggccc tgagccactt      180
ccaggtgatac gtggtcagca acattgcctc caagatggag cacatggtct cctcgttctg      240
tctgatgcgc tgcaggagcg cccaggtggt gcacttgat ggcgccacct acagcgcgga      300
cggggaag                                         308

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<210> 6
<211> 16
<212> PRT
<213> homo sapiens

<400> 6
Phe Thr Met Cys Phe Val Pro Leu Val Cys Trp Val Val Cys Thr Cys
1             5             10             15

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<210> 7
<211> 21
<212> DNA
<213> homo sapiens

<400> 7
gatggacctg ttgcagtgga t                                         21

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<210> 8
<211> 21
<212> DNA
<213> homo sapiens

<400> 8
gaccacgatac acctggaagt g                                         21

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<210> 9
<211> 80
<212> DNA
<213> homo sapiens

<400> 9
tgaagaactc aaaggagccc tgetgcaggg tggagccgtc gctctgagct ttgctttgga      60
tccactgcaa caggtccatc                                         80

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<210> 10
<211> 13
<212> PRT

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<213> homo sapiens

<400> 10

Leu Ser Leu Leu Ile Thr Thr Arg Pro Thr Ala Leu Glu
1 5 10

<210> 11

<211> 13

<212> PRT

<213> homo sapiens

<400> 11

Gly Leu Leu Arg Gln Thr Ser Arg Thr Thr Thr Ala Val
1 5 10

<210> 12

<211> 13

<212> PRT

<213> homo sapiens

<400> 12

Ser Phe Leu Ala Leu Thr Ser Arg Phe Leu Phe Gly Leu
1 5 10

<210> 13

<211> 10

<212> PRT

<213> homo sapiens

<400> 13

Met Asn Gln Ser Ala Thr Glu Cys Ser Met
1 5 10

<210> 14

<211> 514

<212> PRT

<213> homo sapiens

<400> 14

Met Cys Phe Ile Pro Leu Val Cys Trp Ile Val Cys Thr Gly Leu Lys
1 5 10 15

Gln Gln Met Glu Ser Gly Lys Ser Leu Ala Gln Thr Ser Lys Thr Ser
20 25 30

Thr Ala Val Tyr Val Phe Phe Leu Ser Ser Leu Leu Gln Pro Arg Gly
35 40 45

Gly Ser Gln Glu His Gly Leu Cys Ala His Leu Trp Gly Leu Cys Ser
50 55 60

Leu Ala Ala Asp Gly Ile Trp Asn Gln Lys Ile Leu Phe Glu Glu Ser
65 70 75 80

Asp Leu Arg Asn His Gly Leu Gln Lys Ala Asp Val Ser Ala Phe Leu
85 90 95

Pro Asp Cys Lys Leu Gln Val Leu Glu Leu Asp Asn Cys Asn Leu Thr
 420 425 430

Ser His Cys Cys Trp Asp Leu Ser Thr Leu Leu Thr Ser Ser Gln Ser
 435 440 445

Leu Arg Lys Leu Ser Leu Gly Asn Asn Asp Leu Gly Asp Leu Gly Val
 450 455 460

Met Met Phe Cys Glu Val Leu Lys Gln Gln Ser Cys Leu Leu Gln Asn
 465 470 475 480

Leu Gly Leu Ser Glu Met Tyr Phe Asn Tyr Glu Thr Lys Ser Ala Leu
 485 490 495

Glu Thr Leu Gln Glu Glu Lys Pro Glu Leu Thr Val Val Phe Glu Pro
 500 505 510

Ser Trp

<210> 15
 <211> 1429
 <212> PRT
 <213> homo sapiens

<400> 15

Met Ala Gly Gly Ala Trp Gly Arg Leu Ala Cys Tyr Leu Glu Phe Leu
 1 5 10 15

Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
 20 25 30

His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
 35 40 45

Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
 50 55 60

Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
 65 70 75 80

Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
 85 90 95

Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
 100 105 110

Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys
 115 120 125

Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser
 130 135 140

Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu
 145 150 155 160

Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala
 165 170 175

Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro
 180 185 190
 Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu
 195 200 205
 Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg
 210 215 220
 Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
 225 230 235 240
 Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu
 245 250 255
 Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu
 260 265 270
 Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His
 275 280 285
 Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val
 290 295 300
 Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro
 305 310 315 320
 Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala
 325 330 335
 Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly
 340 345 350
 Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser
 355 360 365
 Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile
 370 375 380
 Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser
 385 390 395 400
 Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly
 405 410 415
 Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln
 420 425 430
 Pro Gln Pro Ala Asp Ala Leu Leu Gly Ser Leu Leu Gly Lys Thr Ile
 435 440 445
 Leu Pro Glu Ala Ser Phe Leu Ile Thr Ala Arg Thr Thr Ala Leu Gln
 450 455 460
 Asn Leu Ile Pro Ser Leu Glu Gln Ala Arg Trp Val Glu Val Leu Gly
 465 470 475 480
 Phe Ser Glu Ser Ser Arg Lys Glu Tyr Phe Tyr Arg Tyr Phe Thr Asp
 485 490 495
 Glu Arg Gln Ala Ile Arg Ala Phe Arg Leu Val Lys Ser Asn Lys Glu

	500		505		510
Leu Trp	Ala Leu Cys Leu Val	Pro Trp Val Ser Trp	Leu Ala Cys Thr		
	515	520	525		
Cys Leu	Met Gln Gln Met	Lys Arg Lys Glu Lys	Leu Thr Leu Thr Ser		
	530	535	540		
Lys Thr	Thr Thr Thr	Leu Cys Leu His Tyr	Leu Ala Gln Ala Leu Gln		
	545	550	555		560
Ala Gln	Pro Leu Gly	Pro Gln Leu Arg Asp	Leu Cys Ser Leu Ala Ala		
	565	570	575		
Glu Gly	Ile Trp	Gln Lys Lys Thr	Leu Phe Ser Pro Asp Asp	Leu Arg	
	580		585	590	
Lys His	Gly Leu Asp Gly	Ala Ile Ile Ser Thr	Phe Leu Lys Met Gly		
	595	600	605		
Ile Leu	Gln Glu His Pro	Ile Pro Leu Ser Tyr	Ser Phe Ile His Leu		
	610	615	620		
Cys Phe	Gln Glu Phe Phe	Ala Ala Met Ser Tyr	Val Leu Glu Asp Glu		
	625	630	635		640
Lys Gly	Arg Gly Lys His	Ser Asn Cys Ile Ile	Asp Leu Glu Lys Thr		
	645	650	655		
Leu Glu	Ala Tyr Gly Ile	His Gly Leu Phe Gly	Ala Ser Thr Thr Arg		
	660	665	670		
Phe Leu	Leu Gly Leu Leu Ser	Asp Glu Gly Glu Arg	Glu Met Glu Asn		
	675	680	685		
Ile Phe	His Cys Arg Leu Ser	Gln Gly Arg Asn Leu	Met Gln Trp Val		
	690	695	700		
Pro Ser	Leu Gln Leu Leu Gln	Pro His Ser Leu Glu	Ser Leu His		
	705	710	715	720	
Cys Leu	Tyr Glu Thr Arg	Asn Lys Thr Phe Leu	Thr Gln Val Met Ala		
	725	730	735		
His Phe	Glu Glu Met Gly Met	Cys Val Glu Thr Asp	Met Glu Leu Leu		
	740	745	750		
Val Cys	Thr Phe Cys Ile Lys	Phe Ser Arg His Val	Lys Lys Leu Gln		
	755	760	765		
Leu Ile	Glu Gly Arg Gln His	Arg Ser Thr Trp Ser	Pro Thr Met Val		
	770	775	780		
Val Leu	Phe Arg Trp Val Pro	Val Thr Asp Ala Tyr	Trp Gln Ile Leu		
	785	790	795	800	
Phe Ser	Val Leu Lys Val Thr	Arg Asn Leu Lys Glu	Leu Asp Leu Ser		
	805	810	815		
Gly Asn	Ser Leu Ser His Ser	Ala Val Lys Ser Leu	Cys Lys Thr Leu		
	820	825	830		

Arg Arg Pro Arg Cys Leu Leu Glu Thr Leu Arg Leu Ala Gly Cys Gly
 835 840 845
 Leu Thr Ala Glu Asp Cys Lys Asp Leu Ala Phe Gly Leu Arg Ala Asn
 850 855 860
 Gln Thr Leu Thr Glu Leu Asp Leu Ser Phe Asn Val Leu Thr Asp Ala
 865 870 875 880
 Gly Ala Lys His Leu Cys Gln Arg Leu Arg Gln Pro Ser Cys Lys Leu
 885 890 895
 Gln Arg Leu Gln Leu Val Ser Cys Gly Leu Thr Ser Asp Cys Cys Gln
 900 905 910
 Asp Leu Ala Ser Val Leu Ser Ala Ser Pro Ser Leu Lys Glu Leu Asp
 915 920 925
 Leu Gln Gln Asn Asn Leu Asp Asp Val Gly Val Arg Leu Leu Cys Glu
 930 935 940
 Gly Leu Arg His Pro Ala Cys Lys Leu Ile Arg Leu Gly Leu Asp Gln
 945 950 955 960
 Thr Thr Leu Ser Asp Glu Met Arg Gln Glu Leu Arg Ala Leu Glu Gln
 965 970 975
 Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met
 980 985 990
 Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser
 995 1000 1005
 Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His
 1010 1015 1020
 Val Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe
 1025 1030 1035
 Pro Ile Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro
 1040 1045 1050
 Val Glu Leu Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu
 1055 1060 1065
 His Thr Lys Pro Leu Gly Thr Asp Asp Asp Phe Trp Gly Pro Thr
 1070 1075 1080
 Gly Pro Val Ala Thr Glu Val Val Asp Lys Glu Lys Asn Leu Tyr
 1085 1090 1095
 Arg Val His Phe Pro Val Ala Gly Ser Tyr Arg Trp Pro Asn Thr
 1100 1105 1110
 Gly Leu Cys Phe Val Met Arg Glu Ala Val Thr Val Glu Ile Glu
 1115 1120 1125
 Phe Cys Val Trp Asp Gln Phe Leu Gly Glu Ile Asn Pro Gln His
 1130 1135 1140

Ser	Trp	Met	Val	Ala	Gly	Pro	Leu	Leu	Asp	Ile	Lys	Ala	Glu	Pro
1145						1150					1155			
Gly	Ala	Val	Glu	Ala	Val	His	Leu	Pro	His	Phe	Val	Ala	Leu	Gln
1160						1165					1170			
Gly	Gly	His	Val	Asp	Thr	Ser	Leu	Phe	Gln	Met	Ala	His	Phe	Lys
1175						1180					1185			
Glu	Glu	Gly	Met	Leu	Leu	Glu	Lys	Pro	Ala	Arg	Val	Glu	Leu	His
1190						1195					1200			
His	Ile	Val	Leu	Glu	Asn	Pro	Ser	Phe	Ser	Pro	Leu	Gly	Val	Leu
1205						1210					1215			
Leu	Lys	Met	Ile	His	Asn	Ala	Leu	Arg	Phe	Ile	Pro	Val	Thr	Ser
1220						1225					1230			
Val	Val	Leu	Leu	Tyr	His	Arg	Val	His	Pro	Glu	Glu	Val	Thr	Phe
1235						1240					1245			
His	Leu	Tyr	Leu	Ile	Pro	Ser	Asp	Cys	Ser	Ile	Arg	Lys	Glu	Leu
1250						1255					1260			
Glu	Leu	Cys	Tyr	Arg	Ser	Pro	Gly	Glu	Asp	Gln	Leu	Phe	Ser	Glu
1265						1270					1275			
Phe	Tyr	Val	Gly	His	Leu	Gly	Ser	Gly	Ile	Arg	Leu	Gln	Val	Lys
1280						1285					1290			
Asp	Lys	Lys	Asp	Glu	Thr	Leu	Val	Trp	Glu	Ala	Leu	Val	Lys	Pro
1295						1300					1305			
Gly	Asp	Leu	Met	Pro	Ala	Thr	Thr	Leu	Ile	Pro	Pro	Ala	Arg	Ile
1310						1315					1320			
Ala	Val	Pro	Ser	Pro	Leu	Asp	Ala	Pro	Gln	Leu	Leu	His	Phe	Val
1325						1330					1335			
Asp	Gln	Tyr	Arg	Glu	Gln	Leu	Ile	Ala	Arg	Val	Thr	Ser	Val	Glu
1340						1345					1350			
Val	Val	Leu	Asp	Lys	Leu	His	Gly	Gln	Val	Leu	Ser	Gln	Glu	Gln
1355						1360					1365			
Tyr	Glu	Arg	Val	Leu	Ala	Glu	Asn	Thr	Arg	Pro	Ser	Gln	Met	Arg
1370						1375					1380			
Lys	Leu	Phe	Ser	Leu	Ser	Gln	Ser	Trp	Asp	Arg	Lys	Cys	Lys	Asp
1385						1390					1395			
Gly	Leu	Tyr	Gln	Ala	Leu	Lys	Glu	Thr	His	Pro	His	Leu	Ile	Met
1400						1405					1410			
Glu	Leu	Trp	Glu	Lys	Gly	Ser	Lys	Lys	Gly	Leu	Leu	Pro	Leu	Ser
1415						1420					1425			

Ser

<210> 16

<211> 8
 <212> PRT
 <213> bacteriophage T7

<400> 16

Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 17
 <211> 733
 <212> DNA
 <213> homo sapiens

<400> 17
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 aatctgaggg tgcacggtca gtcttctctt tcccccaaa acccaaggac accctcatga 120
 tctcccgagc tcttgaggtc acatgcgtgg tggaggagct aagccacgaa gacctgagg 180
 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgaggg 240
 aggagcagta caacagcagc taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
 ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccatcg 360
 agaaaacctc ctccaagacc aaagggcagc ccgagaacc acaggtgtac accctgcccc 420
 catcccgagg tgagctgacc aagaaccagg tcagcctgac ctgcctggct aaaggcttct 480
 atccaagcga catcgccgtg gaggaggaga gcaatgggca gccggagaac aactacaaga 540
 ccacgcctcc cgtgctggac tccgacggtc ccttcttctc ctacagcaag ctcaccgtgg 600
 acaagagcag gtggcagcag gggaaactct tctcatgctc cgtgatgcat gaggtctctc 660
 acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
 gactctagag gat 733

<210> 18
 <211> 1034
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Ala Ser Thr Arg Cys Lys Leu Ala Arg Tyr Leu Glu Asp Leu Glu
 1 5 10 15
 Asp Val Asp Leu Lys Lys Phe Lys Met His Leu Glu Asp Tyr Pro Pro
 20 25 30
 Gln Lys Gly Cys Ile Pro Leu Pro Arg Gly Gln Thr Glu Lys Ala Asp
 35 40 45
 His Val Asp Leu Ala Thr Leu Met Ile Asp Phe Asn Gly Glu Glu Lys
 50 55 60

Ala Trp Ala Met Ala Val Trp Ile Phe Ala Ala Ile Asn Arg Arg Asp
 65 70 75 80
 Leu Tyr Glu Lys Ala Lys Arg Asp Glu Pro Lys Trp Gly Ser Asp Asn
 85 90 95
 Ala Arg Val Ser Asn Pro Thr Val Ile Cys Gln Glu Asp Ser Ile Glu
 100 105 110
 Glu Glu Trp Met Gly Leu Leu Glu Tyr Leu Ser Arg Ile Ser Ile Cys
 115 120 125
 Lys Met Lys Lys Asp Tyr Arg Lys Lys Tyr Arg Lys Tyr Val Arg Ser
 130 135 140
 Arg Phe Gln Cys Ile Glu Asp Arg Asn Ala Arg Leu Gly Glu Ser Val
 145 150 155 160
 Ser Leu Asn Lys Arg Tyr Thr Arg Leu Arg Leu Ile Lys Glu His Arg
 165 170 175
 Ser Gln Gln Glu Arg Glu Gln Glu Leu Leu Ala Ile Gly Lys Thr Lys
 180 185 190
 Thr Cys Glu Ser Pro Val Ser Pro Ile Lys Met Glu Leu Phe Asp
 195 200 205
 Pro Asp Asp Glu His Ser Glu Pro Val His Thr Val Val Phe Gln Gly
 210 215 220
 Ala Ala Gly Ile Gly Lys Thr Ile Leu Ala Arg Lys Met Met Leu Asp
 225 230 235 240
 Trp Ala Ser Gly Thr Leu Tyr Gln Asp Arg Phe Asp Tyr Leu Phe Tyr
 245 250 255
 Ile His Cys Arg Glu Val Ser Leu Val Thr Gln Arg Ser Leu Gly Asp
 260 265 270
 Leu Ile Met Ser Cys Cys Pro Asp Pro Asn Pro Pro Ile His Lys Ile
 275 280 285
 Val Arg Lys Pro Ser Arg Ile Leu Phe Leu Met Asp Gly Phe Asp Glu
 290 295 300
 Leu Gln Gly Ala Phe Asp Glu His Ile Gly Pro Leu Cys Thr Asp Trp
 305 310 315 320
 Gln Lys Ala Glu Arg Gly Asp Ile Leu Leu Ser Ser Leu Ile Arg Lys
 325 330 335
 Lys Leu Leu Pro Glu Ala Ser Leu Leu Ile Thr Thr Arg Pro Val Ala
 340 345 350
 Leu Glu Lys Leu Gln His Leu Leu Asp His Pro Arg His Val Glu Ile
 355 360 365
 Leu Gly Phe Ser Glu Ala Lys Arg Lys Glu Tyr Phe Phe Lys Tyr Phe
 370 375 380
 Ser Asp Glu Ala Gln Ala Arg Ala Ala Phe Ser Leu Ile Gln Glu Asn

385	390	395	400
Glu Val Leu Phe Thr Met Cys Phe Ile	Pro Leu Val Cys Trp Ile Val		
405	410	415	
Cys Thr Gly Leu Lys Gln Gln Met	Glu Ser Gly Lys Ser Leu Ala Gln		
420	425	430	
Thr Ser Lys Thr Thr Thr Ala Val Tyr Val Phe Phe Leu Ser Ser Leu			
435	440	445	
Leu Gln Pro Arg Gly Gly Ser Gln Glu His Gly Leu Cys Ala His Leu			
450	455	460	
Trp Gly Leu Cys Ser Leu Ala Ala Asp Gly Ile Trp Asn Gln Lys Ile			
465	470	475	480
Leu Phe Glu Glu Ser Asp Leu Arg Asn His Gly Leu Gln Lys Ala Asp			
485	490	495	
Val Ser Ala Phe Leu Arg Met Asn Leu Phe Gln Lys Glu Val Asp Cys			
500	505	510	
Glu Lys Phe Tyr Ser Phe Ile His Met Thr Phe Gln Glu Phe Phe Ala			
515	520	525	
Ala Met Tyr Tyr Leu Leu Glu Glu Glu Lys Glu Gly Arg Thr Asn Val			
530	535	540	
Pro Gly Ser Arg Leu Lys Leu Pro Ser Arg Asp Val Thr Val Leu Leu			
545	550	555	560
Glu Asn Tyr Gly Lys Phe Glu Lys Gly Tyr Leu Ile Phe Val Val Arg			
565	570	575	
Phe Leu Phe Gly Leu Val Asn Gln Glu Arg Thr Ser Tyr Leu Glu Lys			
580	585	590	
Lys Leu Ser Cys Lys Ile Ser Gln Gln Ile Arg Leu Glu Leu Leu Lys			
595	600	605	
Trp Ile Glu Val Lys Ala Lys Ala Lys Lys Leu Gln Ile Gln Pro Ser			
610	615	620	
Gln Leu Glu Leu Phe Tyr Cys Leu Tyr Glu Met Gln Glu Glu Asp Phe			
625	630	635	640
Val Gln Arg Ala Met Asp Tyr Phe Pro Lys Ile Glu Ile Asn Leu Ser			
645	650	655	
Thr Arg Met Asp His Met Val Ser Ser Phe Cys Ile Glu Asn Cys His			
660	665	670	
Arg Val Glu Ser Leu Ser Leu Gly Phe Leu His Asn Met Pro Lys Glu			
675	680	685	
Glu Glu Glu Glu Glu Lys Glu Gly Arg His Leu Asp Met Val Gln Cys			
690	695	700	
Val Leu Pro Ser Ser Ser His Ala Ala Cys Ser His Gly Leu Val Asn			
705	710	715	720

Ser His Leu Thr Ser Ser Phe Cys Arg Gly Leu Phe Ser Val Leu Ser
 725 730 735
 Thr Ser Gln Ser Leu Thr Glu Leu Asp Leu Ser Asp Asn Ser Leu Gly
 740 745 750
 Asp Pro Gly Met Arg Val Leu Cys Glu Thr Leu Gln His Pro Gly Cys
 755 760 765
 Asn Ile Arg Arg Leu Trp Leu Gly Arg Cys Gly Leu Ser His Glu Cys
 770 775 780
 Cys Phe Asp Ile Ser Leu Val Leu Ser Ser Asn Gln Lys Leu Val Glu
 785 790 800
 Leu Asp Leu Ser Asp Asn Ala Leu Gly Asp Phe Gly Ile Arg Leu Leu
 805 810 815
 Cys Val Gly Leu Lys His Leu Leu Cys Asn Leu Lys Lys Leu Trp Leu
 820 825 830
 Val Ser Cys Cys Leu Thr Ser Ala Cys Cys Gln Asp Leu Ala Ser Val
 835 840 845
 Leu Ser Thr Ser His Ser Leu Thr Arg Leu Tyr Val Gly Glu Asn Ala
 850 855 860
 Leu Gly Asp Ser Gly Val Ala Ile Leu Cys Glu Lys Ala Lys Asn Pro
 865 870 875 880
 Gln Cys Asn Leu Gln Lys Leu Gly Leu Val Asn Ser Gly Leu Thr Ser
 885 890 895
 Val Cys Cys Ser Ala Leu Ser Ser Val Leu Ser Thr Asn Gln Asn Leu
 900 905 910
 Thr His Leu Tyr Leu Arg Gly Asn Thr Leu Gly Asp Lys Gly Ile Lys
 915 920 925
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